GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: March 14, 2003, 05:30:50 ; Search time 1.75281 Seconds
(without alignments)
1057.973 Million cell updates/sec

Title: US-09-698-781-17
Perfect score: 44
Sequence: 1 TLFPVLLFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	100.0	203	4	Q9H108	Q9h108 homo sapien
2	39	88.6	421	2	Q9F0X9	Q9f0x9 pseudomonas
3	37	84.1	604	8	Q8W9G3	Q8w9g3 tachyglossu
4	36	81.8	85	2	O85399	O85399 coxiella bu
5	36	81.8	161	16	Q9KNN5	Q9knn5 vibrio chol
6	36	81.8	227	8	Q9TBK7	Q9tbk7 guira guira
7	36	81.8	408	3	O94639	O94639 schizosacch
8	35	79.5	222	16	Q9X0H3	Q9x0h3 thermotoga
9	35	79.5	227	8	Q9B6Y8	Q9b6y8 casuarius b
10	35	79.5	316	17	Q8TRD3	Q8trd3 methanosarc
11	35	79.5	361	16	Q9WYL9	Q9wyl9 thermotoga
12	35	79.5	501	16	Q98EG2	Q98eg2 rhizobium l
13	35	79.5	543	16	Q99VT7	Q99vt7 staphylococ
14	35	79.5	543	16	Q932E9	Q932e9 staphylococ
15	35	79.5	622	13	O57661	O57661 xenopus lae
16	35	79.5	826	2	Q8RPN1	Q8rpn1 ehrlichia c
17	35	79.5	1325	10	O64533	O64533 arabidopsis
18	34	77.3	174	16	O67603	O67603 aquifex aeo
19	34	77.3	177	11	Q9CWD1	Q9cwd1 mus musculu
20	34	77.3	227	8	Q9XL19	Q9xl19 smithornis
21	34	77.3	237	16	Q9K8B8	Q9k8b8 bacillus ha
22	34	77.3	246	11	Q9D3M3	Q9d3m3 mus musculu
23	34	77.3	247	4	Q9H953	Q9h953 homo sapien
24	34	77.3	247	11	Q9DAV4	Q9dav4 mus musculu
25	34	77.3	247	11	Q9CR67	Q9cr67 mus musculu
26	34	77.3	326	2	Q93QC8	Q93qc8 carnobacter
27	34	77.3	330	5	Q9TXH3	Q9txh3 caenorhabdi
28	34	77.3	341	8	Q95BA4	Q95ba4 flaveria ra
29	34	77.3	356	16	Q97J84	Q97j84 clostridium
30	34	77.3	369	16	Q8RD02	Q8rd02 thermoanaer
31	34	77.3	373	16	Q8RAJ8	Q8raj8 thermoanaer
32	34	77.3	405	16	Q99SZ8	Q99sz8 staphylococ
33	34	77.3	405	16	Q931N2	Q931n2 staphylococ
34	34	77.3	455	2	Q9X479	Q9x479 enterococcu
35	34	77.3	471	2	Q93MR9	Q93mr9 myxococcus
36	34	77.3	511	16	Q8YYJ9	Q8yyj9 anabaena sp
37	34	77.3	653	16	Q9HTG5	Q9htg5 pseudomonas
38	34	77.3	1118	5	Q9N8Z4	Q9n8z4 trypanosoma
39	33	75.0	89	16	Q9CF15	Q9cf15 lactococcus
40	33	75.0	101	4	Q9UPH8	Q9uph8 homo sapien
41	33	75.0	119	16	Q8XXQ1	Q8xxq1 ralstonia s
42	33	75.0	186	16	Q8XYL2	Q8xyl2 ralstonia s
43	33	75.0	250	4	Q8WU77	Q8wu77 homo sapien
44	33	75.0	251	4	O75549	O75549 homo sapien
45	33	75.0	290	16	Q9CMA0	Q9cma0 pasteurella

ALIGNMENTS

RESULT 1
Q9H108
ID Q9H108 PRELIMINARY; PRT; 203 AA.
AC Q9H108;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DJ417L20.1 (Cysteine-rich secretory protein 3 (Crisp-3, SGP28))
DE (Fragment).
GN DJ417L20.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillimore B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL121974; CAC19654.1; -.
DR HSSP; P04284; 1CFE.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
DR PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
FT NON_TER 203 203
SQ SEQUENCE 203 AA; 22912 MW; F80D707EE0D81A2B CRC64;

Query Match 100.0%; Score 44; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLFPVLLFL 9
|||||||||
Db 2 TLFPVLLFL 10

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RESULT 2
Q9F0X9
ID   Q9F0X9      PRELIMINARY;      PRT;   421 AA.
AC   Q9F0X9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Putative nitrate/nitrite transporter.
GN   NARD.
OS   Pseudomonas fluorescens.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=294;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C7R12;
RX   MEDLINE=21240335; PubMed=11342223;
RA   Philippot L., Mirleau P., Mazurier S., Siblot S., Hartmann A.,
RA   Lemanceau P., Germon J.C.;
RT   "Characterization and transcriptional analysis of Pseudomonas
RT   fluorescens denitrifying clusters containing the nar, nir, nor and nos
RT   genes.";
RL   Biochim. Biophys. Acta 1517:436-440(2001).
DR   EMBL; AF197465; AAG34371.1; -.
SQ   SEQUENCE   421 AA;  46035 MW;  4D8482587EBA1861 CRC64;

  Query Match             88.6%;  Score 39;  DB 2;  Length 421;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TLFPVLLFL 9
             |||||:||:
Db     314 TLFPVILFV 322


RESULT 3
Q8W9G3
ID   Q8W9G3      PRELIMINARY;      PRT;   604 AA.
AC   Q8W9G3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   NADH dehydrogenase subunit 5.
GN   NADH5.
OS   Tachyglossus aculeatus (Australian echidna).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Monotremata; Tachyglossidae; Tachyglossus.
OX   NCBI_TaxID=9261;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=21592585; PubMed=11734900;
RA   Janke A., Magnell O., Wieczorek G., Westerman M., Arnason U.;
RT   "Phylogenetic analysis of 18S rRNA and the mitochondrial genomes of
RT   the wombat, Vombatus ursinus, and the spiny anteater, Tachyglossus
RT   aculeatus: Increased Support for the Marsupionta Hypothesis.";
RL   J. Mol. Evol. 54:71-80(2002).
DR   EMBL; AJ303116; CAC88020.1; -.
DR   InterPro; IPR003916; NADHub_oxred5.
DR   InterPro; IPR001750; Oxidored_q1.
DR   InterPro; IPR001516; Oxidored_q1_N.
DR   Pfam; PF00361; oxidored_q1; 1.
DR   Pfam; PF00662; oxidored_q1_N; 1.
DR   PRINTS; PR01434; NADHDHGNASE5.
KW   Mitochondrion.
SQ   SEQUENCE   604 AA;  67629 MW;  9624D7B3A3F54486 CRC64;

  Query Match             84.1%;  Score 37;  DB 8;  Length 604;
  Best Local Similarity   77.8%;  Pred. No. 65;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TLFPVLLFL 9
             :|||:||||
Db      48 SLFPLLLFL 56


RESULT 4
O85399
ID   O85399      PRELIMINARY;      PRT;    85 AA.
AC   O85399;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 10.1 kDa protein.
OS   Coxiella burnetii.
OC   Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC   Coxiella group; Coxiella.
OX   NCBI_TaxID=777;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NINE MILE PHASE I;
RX   MEDLINE=98348442; PubMed=9683477;
RA   Willems H., Jaeger C., Baljer G.;
RT   "Physical and genetic map of the obligate intracellular bacterium
RT   Coxiella burnetii.";
RL   J. Bacteriol. 180:3816-3822(1998).
DR   EMBL; AF064956; AAD09940.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   85 AA;  10146 MW;  8F67FC9780CD1E2A CRC64;

  Query Match             81.8%;  Score 36;  DB 2;  Length 85;
  Best Local Similarity   77.8%;  Pred. No. 20;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TLFPVLLFL 9
             | ||:||||
Db      25 TAFPLLLFL 33


RESULT 5
Q9KNN5
ID   Q9KNN5      PRELIMINARY;      PRT;   161 AA.
AC   Q9KNN5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FxsA protein.
GN   VC2696.
OS   Vibrio cholerae.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX   NCBI_TaxID=666;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EL TOR N16961 / SEROTYPE O1;
RX   MEDLINE=20406833; PubMed=10952301;
RA   Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA   Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA   Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA   Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA   McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA   Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA   Fraser C.M.;
RT   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT   cholerae.";
RL   Nature 406:477-483(2000).
DR   EMBL; AE004335; AAF95837.1; -.
DR   TIGR; VC2696; -.
KW   Complete proteome.
SQ   SEQUENCE   161 AA;  17485 MW;  04BD915C81FBEB22 CRC64;

  Query Match             81.8%;  Score 36;  DB 16;  Length 161;
  Best Local Similarity   75.0%;  Pred. No. 33;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 LFPVLLFL 9
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          :||:||||
Db      1 MFPILLFL 8


RESULT 6
Q9TBK7
ID   Q9TBK7      PRELIMINARY;      PRT;   227 AA.
AC   Q9TBK7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ATP synthase A chain (EC 3.6.1.34).
OS   Guira guira (Guira cuckoo).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Cuculiformes; Crotophagidae; Guira.
OX   NCBI_TaxID=30392;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99416451; PubMed=10486983;
RA   Hughes J.M., Baker A.J.;
RT   "Phylogenetic relationships of the enigmatic hoatzin (Opisthocomus
RT   hoazin) resolved using mitochondrial and nuclear gene sequences.";
RL   Mol. Biol. Evol. 16:1300-1307(1999).
CC   -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC       DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC       CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC       SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC       HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
DR   EMBL; AF168018; AAD56446.1; -.
DR   HSSP; P00855; 1C17.
DR   InterPro; IPR000568; ATPsynt_Asub.
DR   Pfam; PF00119; ATP-synt_A; 1.
DR   PRINTS; PR00123; ATPASEA.
DR   TIGRFAMs; TIGR01131; ATP_synt_6_or_A; 1.
DR   PROSITE; PS00449; ATPASE_A; 1.
KW   CF(0); Hydrogen ion transport; Mitochondrion; Transmembrane.
SQ   SEQUENCE   227 AA;  25096 MW;  49472AE8A92F0195 CRC64;

  Query Match             81.8%;  Score 36;  DB 8;  Length 227;
  Best Local Similarity   87.5%;  Pred. No. 44;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TLFPVLLF 8
            |||| |||
Db      24 TLFPALLF 31


RESULT 7
O94639
ID   O94639      PRELIMINARY;      PRT;   408 AA.
AC   O94639;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative transporter C16D10.06.
GN   SPBC16D10.06.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Brown D., Churcher C.M.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- SIMILARITY: TO YEAST ZRT1.
DR   EMBL; AL035637; CAB38510.1; -.
DR   InterPro; IPR004698; ZIP_transport.
DR   InterPro; IPR003689; Zn_trnprt_Zip.
DR   Pfam; PF02535; Zip; 1.
DR   TIGRFAMs; TIGR00820; zip; 1.
KW   Hypothetical protein; Transmembrane; Transport.
FT   TRANSMEM     64     84        POTENTIAL.
FT   TRANSMEM    141    161        POTENTIAL.
FT   TRANSMEM    279    299        POTENTIAL.
FT   TRANSMEM    315    335        POTENTIAL.
SQ   SEQUENCE   408 AA;  45272 MW;  0EBC0AF53CC3F0CE CRC64;

  Query Match             81.8%;  Score 36;  DB 3;  Length 408;
  Best Local Similarity   75.0%;  Pred. No. 72;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TLFPVLLF 8
            |||||::|
Db     281 TLFPVIIF 288


RESULT 8
Q9X0H3
ID   Q9X0H3      PRELIMINARY;      PRT;   222 AA.
AC   Q9X0H3;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein TM1087.
GN   TM1087.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MSB8 / DSM 3109;
RX   MEDLINE=99287316; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
DR   EMBL; AE001768; AAD36164.1; -.
DR   TIGR; TM1087; -.
DR   InterPro; IPR002610; Rhomboid.
DR   Pfam; PF01694; Rhomboid; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   222 AA;  25929 MW;  727793AEC17C6E50 CRC64;

  Query Match             79.5%;  Score 35;  DB 16;  Length 222;
  Best Local Similarity   66.7%;  Pred. No. 66;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TLFPVLLFL 9
            ||||:  ||
Db     156 TLFPIFFFL 164


RESULT 9
Q9B6Y8
ID   Q9B6Y8      PRELIMINARY;      PRT;   227 AA.
AC   Q9B6Y8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ATP synthase A chain (EC 3.6.1.34).
OS   Casuarius bennetti (Dwarf cassowary), and
OS   Casuarius casuarius (Australian cassowary) (Double-wattled cassowary).
OG   Mitochondrion.
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Palaeognathae; Casuariiformes; Casuariidae;
OC   Casuarius.
OX   NCBI_TaxID=30463, 8787;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=C.bennetti; TISSUE=MUSCLE;
RX   MEDLINE=21085666; PubMed=11217857;
RA   Cooper A., Lalueza-Fox C., Anderson S., Rambaut A., Austin J.,
RA   Ward R.;
RT   "Complete mitochondrial genome sequences of two extinct moas clarify
RT   ratite evolution.";
RL   Nature 409:704-707(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=C.casuarius;
RX   MEDLINE=21263106; PubMed=11370967;
RA   Haddrath O., Baker A.J.;
RT   "Complete mitochondrial DNA geonome sequences of extinct birds: ratite
RT   phylogenetics and the vicariance biogeography hypothesis.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 268:939-945(2001).
CC   -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC       DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC       CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC       SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC       HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
DR   EMBL; AY016011; AAK08558.1; -.
DR   EMBL; AF338713; AAK53319.1; -.
DR   InterPro; IPR000568; ATPsynt_Asub.
DR   Pfam; PF00119; ATP-synt_A; 1.
DR   PRINTS; PR00123; ATPASEA.
DR   TIGRFAMs; TIGR01131; ATP_synt_6_or_A; 1.
DR   PROSITE; PS00449; ATPASE_A; 1.
KW   CF(0); Hydrogen ion transport; Mitochondrion; Transmembrane.
SQ   SEQUENCE   227 AA;  24981 MW;  9A5ADD8ED08BFBC3 CRC64;

  Query Match             79.5%;  Score 35;  DB 8;  Length 227;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 LFPVLLF 8
           |||||||
Db      25 LFPVLLF 31


RESULT 10
Q8TRD3
ID   Q8TRD3      PRELIMINARY;      PRT;   316 AA.
AC   Q8TRD3;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Oligopeptide ABC transporter, permease.
GN   OPPB OR MA1247.
OS   Methanosarcina acetivorans.
OC   Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2214;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C2A / ATCC 35395 / DSM 2834;
RX   MEDLINE=21929760; PubMed=11932238;
RA   Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA   FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA   Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA   Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA   Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA   Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA   Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA   Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA   Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA   Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA   Metcalf W.W., Birren B.;
RT   "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT   and physiological diversity.";
RL   Genome Res. 12:532-542(2002).
DR   EMBL; AE010792; AAM04666.1; -.
KW   Complete proteome.
SQ   SEQUENCE   316 AA;  35015 MW;  3FA23DB0D54F70D9 CRC64;

  Query Match             79.5%;  Score 35;  DB 17;  Length 316;
  Best Local Similarity   75.0%;  Pred. No. 89;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 LFPVLLFL 9
           |||||:|:
Db      13 LFPVLIFI 20


RESULT 11
Q9WYL9
ID   Q9WYL9      PRELIMINARY;      PRT;   361 AA.
AC   Q9WYL9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein TM0388.
GN   TM0388.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MSB8 / DSM 3109;
RX   MEDLINE=99287316; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
DR   EMBL; AE001718; AAD35473.1; -.
DR   TIGR; TM0388; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   361 AA;  41105 MW;  72967E8C49D323DA CRC64;

  Query Match             79.5%;  Score 35;  DB 16;  Length 361;
  Best Local Similarity   75.0%;  Pred. No. 99;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 LFPVLLFL 9
           |||:||:|
Db      25 LFPILLYL 32


RESULT 12
Q98EG2
ID   Q98EG2      PRELIMINARY;      PRT;   501 AA.
AC   Q98EG2;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein mll4258.
GN   MLL4258.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; AP003003; BAB50957.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   501 AA;  54314 MW;  E70D4239D0C3A929 CRC64;

  Query Match             79.5%;  Score 35;  DB 16;  Length 501;
  Best Local Similarity   77.8%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TLFPVLLFL 9
            :||| ||||
Db      28 SLFPCLLFL 36


RESULT 13
Q99VT7
ID   Q99VT7      PRELIMINARY;      PRT;   543 AA.
AC   Q99VT7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein SA0639.
GN   SA0639.
OS   Staphylococcus aureus (strain N315).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Staphylococcus.
OX   NCBI_TaxID=158879;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
RA   Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA   Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA   Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA   Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA   Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003131; BAB41872.1; -.
DR   HSSP; P13569; 1NBD.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR001140; ABCtranprtrTM.
DR   InterPro; IPR003439; ABC_transportr.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transportr; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   543 AA;  61908 MW;  F74F7863EF364B21 CRC64;

  Query Match             79.5%;  Score 35;  DB 16;  Length 543;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 LFPVLLFL 9
            :||||:||
Db      13 IFPVLMFL 20


RESULT 14
Q932E9
ID   Q932E9      PRELIMINARY;      PRT;   543 AA.
AC   Q932E9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein SAV0684.
GN   SAV0684.
OS   Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC   Staphylococcus.
OX   NCBI_TaxID=158878;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003360; BAB56846.1; -.
DR   InterPro; IPR001140; ABCtranprtrTM.
DR   InterPro; IPR003439; ABC_transportr.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transportr; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   543 AA;  61909 MW;  754E8CBF3458AB25 CRC64;

  Query Match             79.5%;  Score 35;  DB 16;  Length 543;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 LFPVLLFL 9
            :||||:||
Db      13 IFPVLMFL 20


RESULT 15
O57661
ID   O57661      PRELIMINARY;      PRT;   622 AA.
AC   O57661;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Intestinal sodium/LITHIUM-dependent dicarboxylate transporter
DE   (NA(+)/dicarboxylate cotransporter).
GN   NADC-2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=INTESTINE;
RX   MEDLINE=97423461; PubMed=9277403;
RA   Bai L., Pajor A.M.;
RT   "Expression cloning of NaDC-2, an intestinal Na(+)- or Li(+)-dependent
RT   dicarboxylate transporter.";
RL   Am. J. Physiol. 273:G267-G274(1997).
CC   -!- FUNCTION: TRANSPORTS DI- AND TRICARBOXYLATES, INCLUDING SUCCINATE,
CC       CITRATE, AND GLUTARATE, BUT EXCLUDES THE MONOCARBOXYLATE LACTATE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE INTESTINE.
DR   EMBL; U87318; AAB97879.1; -.
DR   InterPro; IPR001898; Na/sulf_symp.
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DR   Pfam; PF00939; Na_sulph_symp; 1.
DR   PROSITE; PS01271; NA_SULFATE; FALSE_NEG.
KW   Transport; Transmembrane; Sodium transport; Symport.
FT   TRANSMEM      13      33       POTENTIAL.
FT   TRANSMEM      53      73       POTENTIAL.
FT   TRANSMEM     114     134       POTENTIAL.
FT   TRANSMEM     259     279       POTENTIAL.
FT   TRANSMEM     299     319       POTENTIAL.
FT   TRANSMEM     366     386       POTENTIAL.
FT   TRANSMEM     411     431       POTENTIAL.
FT   TRANSMEM     456     476       POTENTIAL.
FT   TRANSMEM     494     514       POTENTIAL.
FT   TRANSMEM     542     562       POTENTIAL.
FT   TRANSMEM     584     604       POTENTIAL.
FT   DOMAIN       123     126       POLY-LEU.
FT   CARBOHYD     617     617       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   622 AA;  68550 MW;  D25C06BB806B0098 CRC64;

  Query Match             79.5%;  Score 35;  DB 13;  Length 622;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 LFPVLLF 8
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Db      61 LFPVLLF 67


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Job time : 4.75281 secs
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